



Table IV: HLA Class I Standard Peptide Binding Affinity.

ALLEL	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	2109	25
A*0201	941.01	FLPSDYFPSV	2110	5.0
A*0202	941.01	FLPSDYFPSV	2111	4.3
A*0203	941.01	FLPSDYFPSV	2112	10
A*0205	941.01	FLPSDYFPSV	2113	4.3
A*0206	941.01	FLPSDYFPSV	2114	3.7
A*0207	941.01	FLPSDYFPSV	2115	23
A*6802	1072.34	YVIKVSARV	2116	8.0
A*0301	941.12	KVFPYALINK	2117	11
A*1101	940.06	AVDLYHFLK	2118	6.0
A*3101	941.12	KVFPYALINK	2119	18
A*3301	1083.02	STLPETYYVRR	2120	29
A*6801	941.12	KVFPYALINK	2121	8.0
A*2402	979.02	AYIDNYNKF	2122	12
B*0702	1075.23	APRTLVYLL	2123	5.5
B*3501	1021.05	FPFKYAAAF	2124	7.2
B51	1021.05	FPFKYAAAF	2125	5.5
B*5301	1021.05	FPFKYAAAF	2126	9.3
B*5401	1021.05	FPFKYAAAF	2127	10

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TECH CENTER 1600/2900



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Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	SEQ ID	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	2128	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	2129	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	2130	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	2131	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	2132	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	2133	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	2134	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	2135	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	2136	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	2137	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	2138	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	2139	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2 $\beta$ 1	507.02	2140	GRTQDENPVVHFFK NIVTPRTPPP	9.1
DRB3*0101	DR52a	511	2141	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	2142	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2 $\beta$ 2	553.01	2143	QYIKANSKFIGITE	20

*had clock*

The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.



Table XIX  
CEA DR Super Motif Peptides with

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Table XIX  
CEA DR Super Motif Peptides with



Table XIX CEA DR Super Motif Peptides with Binding

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw33
IFWQRLLLT	1962	RWCIPWQRLLLTASL	1815	0.0110	0.0700	-0.0004		
WQRLLTTA	1963	CIPWQRLLLTASLLT	1816					
LLTASLLT	1964	WQRLLLTASLLTFW	1817					
LLTASLLTF	1965	QRLLTASLLTFWNP	1818			-0.0013		
LTASLLTF	1966	RLLLTASLLTFWNPP	1819					
LTFWNPPT	1967	ASLLTTFWNPPTTAKL	1820					
FWNPPTTA	1968	LLTFWNPPTTAKLTI	1821					
WNPPTTAK	1969	LTFWNPPTTAKLTIE	1822					
LTIESTP FN	1970	TAKLTIESTP FNVAE	1823					
LLVHNLPQ	1971	EVLLVHNLPQHLFG	1824					
LVHNLPQH	1972	VLLVHNLPQHLFGY	1825					
YKGERV DVG	1973	YSWYKGERV DGNRQ	1826					
IGYVIGTQ	1974	NRQIGYVIGTQQT	1827					
IGTQQATPG	1975	GYVIGTQQATPGPAY	1828					
YSGREIY P	1976	GPA YSGREIY PNAS	1829					
IIYPNASL L	1977	GREIY PNASL LION	1830			0.5600	0.0083	
IIYPNASL L	1978	REIYPNASL LIONI	1831					
YPNASL LQ	1979	EIYPNASL LQNI	1832			0.1600	0.0029	
LIIQNIQ N	1980	NASLIIQNIQNDTG	1833			-0.0013		
LIIQNIQND	1981	ASLIIQNIQNDTG F	1834					
IQNIDTGF Y	1982	IQNIIQNDTGFYTLH	1835					
FYTLLHVIKS	1983	DTGFYTLLHVIKSDL V	1836					
YTLHVIKSD	1984	TGFYTLLHVIKSDL V	1837					
LHVIKSDL V	1985	FYTLLHVIKSDL VNEE	1838					
VIKSDL VNE	1986	TLHVIKSDL VNEEAT	1839					
IKSDL VNEE	1987	LHVIKSDL VNEEATG	1840					
LVNEEATG	1988	KSDL VNEEATGQFRV	1841					
VNEEATGQ	1989	SDL VNEEATGQFRVY	1842					
VYPELPKP	1990	QFRVYPELPKPSS	1843					
LPKPSI SSN	1991	YPELPKPSSINNISK	1844			-0.0013		
ISSNNISKPV	1992	KPSI SSNNISKPV	1845			0.0033		
VEDKDAVA	1993	SKPV EKDVAFTCE	1846					
WVNNSQSLP	1994	YLWVNNSQSLPVSP	1847					
WNNOSL PV	1995	LWVNNSQSLPVSP	1848					
LTLFNVTR	1996	NRTLTLFNVTRNDTA	1849					
VTRNDTAS	1997	LFNVTRNDTASYKCE	1850					
V SARRSDS	1998	QNPVSARRSDSVLN	1851					
WLNVL YGP	1999	SDSVLNVL YGP DAP	1852					
LYGPDA PTI	2000	LNVL YGP DAP TISPL	1853					
YGPDA PTIS	2001	NVL YGP DAP TISPL N	1854					
ISPLNTSYR	2002	APLISPLNTSYRSGE	1855					
LSCHA ASN	2003	NLNLSCHA ASN PPAQ	1856					
WFYNGT FQ	2004	QYSWFVNCTFOQST	1857					
LEIPNITYN	2005	QELEIPNITYNNSG	1858					
IPNITVNN	2006	QELIPNITYNNSGSY	1859					
IPNITVNN	2007	ELIPNITYNNSGSY	1860					

most common

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Table XIX CEA DR Super Motif Peptides with Binding

Core Sequence	SeqID Num	Exemplary Sequence	SeqID Num	Exemplary SeqID Num	DR7	DR6w19	DR8w2	DR9	DRw53
ITVNNNSGSY	2008	IPNITV/NNSGSYTCQ	1861						
VNNNSGSY	2009	NITVNNNSGSYTCQAH	1862						
LNRTTVTTI	2010	DTGILNRTTVTTI	1863						0.0088
VTTITVYAE	2011	RTTVTTIYVYAEPK	1864						
VYAEPKPK	2012	TITVYAEPPKPKFTS	1865						
ITSNNNSNPV	2013	KPFITSNNNSNPVDE	1866						-0.0013
VEDEDAVA	2014	SNPYVEDEDAVAVTCE	1867						
LTLLSVTR	2015	NRTLTLSVTRNDVG	1868						0.0021
VTRNDVGP	2016	LLSVTRNDVGPYECC	1869						
VGPyECCG	2017	RNDVGPyECCGQNEL	1870						
IQNELSVDH	2018	ECGQNELSVDHSDP	1871						
LSVDHSDP	2019	QNELSVDHSDPVILN	1872						
VDHSDPVIL	2020	ELSVDHSDPVILNVL	1873						
VILNVLYGP	2021	SDPVILNVLYGDDP	1874						
YGPDDPTIS	2022	NVLYGDDPTISPY	1875						
ISPSYTYYR	2023	DPTISPYTYYRPGV	1876						
YYYRPGV	2024	SPSYTYYRPGVNL	1877						
YYRPGVNL	2025	SYTYYRPGVNLSLSC	1878						
VNLSLSCH	2026	RPGVNLSLSCHAASN	1879						
LSCHAASN	2027	NLSLSCHAASNPPAQ	1880						
LIDGNIQQH	2028	YSWLDGNIQQHQE	1881						
LFISNITEK	2029	TQELFISNITEKNSG	1882						
FISNITEKN	2030	QELFISNITEKNSGL	1883						
ITEKNSGLY	2031	ISNITEKNSQLYTCQ	1884						
LYTCOANN	2032	NSGLYTQOANNSAS	1885						
VKTITVSAE	2033	RTTVKTITVSAELPK	1886						
VSAELPKP	2034	TITVSAELPKPSII	1887						
LPKPSISSN	2035	SAELPKPSISSNNSK	1888						
WNGQSLP	2036	YLWWVNGQSLPVSP	1889						
VNGQSLPV	2037	LWWVNGQSLPVSPR	1890						
LTLFNVTR	2038	NRTTLFNVNTRNDAR	1891						
VTRNDARA	2039	LFNVNTRNDARA YVC	1892						
IQNSY SAN	2040	VCGIQNSY SANRSDP	1893						
VSA NRS DP	2041	QNSVSA NRS DPVTL	1894						
VTL DVL YG	2042	SDPVTL DVL YGPDTP	1895						
LYGPDTP II	2043	LDVL YGPDTPISPP	1896						
YGPDT PIS	2044	DVL YGPDTPISPPD	1897						
ISPPDSSY	2045	TPISPPDSSYLSGA	1898						
LSGANLNL	2046	SSYLSGANLNL SCHS	1899						
LSCHS ASN	2047	NLNLSCHS ASN NSPQ	1900						
WRINGIPQO	2048	OYSWRINGIPQQHTQ	1901						
IPQQHTQVL	2049	INGIPQQHTQVLFIA	1902						
LFI AKITP N	2050	TQVFLIAKITPNNING	1903						0.0038
FAKITP NN	2051	QVLFLIAKITPNNINGT	1904						0.0024
IAKITP NN	2052	VLFIAKITPNNINGT	1905						
YACFVSNL	2053	NGTYACFVSNLATG	1906						

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Table XIX CEA DR Super Motif Peptides with Binding

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Exemplary DR6w19	DR7	DR8w2	DR9	DRw53
FVSNLATG	2054	YACFVSNLATGRNN	1907	0.0070				
VSNLATGR	2055	ACFVSNLATGRNNSI	1908					
IVKSITVSA	2056	NNSIIVKSITVSAASGT	1909	0.00690	0.0370	0.0120		
VKSITVSA	2057	NSIIVKSITVSAASGT	1910	0.0460	0.0760	0.0170		
ITVSAASGT	2058	VKSITVSAASGTSPGL	1911					
VSASGTSP	2059	SITVSAASGTSPGLSA	1912					
LSAGATVGI	2060	SPGLSAGATVGI	1913					
IMIGVLYGV	2061	TYGIMIGVLYGV	1914					
LTIESTPFN	2062	TAKLTIESTPFNVAE	1915					
YKGERVDG	2063	YSWYKGERVDGNRQ	1916					
LPVSPRLQ	2064	NOSLPVSPRLQLSNG	1917					
LNLSCHAA	2065	GENLNLSCHAAASNPP	1918					
LPVSPRLQ	2066	CQSLPVSPLQLSNG	1919					

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and

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Table XIXa  
Exemplary  
Sequence

Core Sequence	Core SeqID Num	Exemplary Sequence	CEA DR 3a Motif Peptides with Binding <sup>2</sup>	-0.0008
Exemplary Position	Exemplary SeqID Num	DR1 DR2w2B1 DR2w2B2 DR3 DR4w4 DR4w5 DR5w11 DR5w12	-0.0008	
IQNDTGFYT	2067	QNIIQNDTGFYTLLHV	110	0.0044 0.0105
IKSDLVNEE	2068	LHVIKSDLVNEEATG	122	0.3200 -0.0055
LVNEEATGQ	2069	KSDLVNEEATGQFRV	126	0.1300 0.0058
VNEEATGQF	2070	SDLVNEEATGQFRVY	127	-
VYPELPKPS	2071	QFRVYPELPKPSISS	137	-
FTCEPETQD	2072	AVAFTCCEPETQDATY	162	-
YKCETQNPV	2073	TASYKCETONPYSAR	210	-
YGPDAPTIS	2074	NVLYGPDADPTISPLN	227	-
VYAEPPKPF	2075	TITVYAEPPKFITS	315	0.0042
VEDEDAVAL	2076	SNPVEDEDAVALTCE	329	0.0054
LTCPEPIQN	2077	AVALTCEPEIQNTY	332	0.0039
IQNELSVDH	2078	ECCIQNELSVDHSDP	340	-
LSVDHSDPV	2079	QNELSVDHSDPVILN	392	0.0820
YGPDDPTIS	2080	NVLYGPDADPTISPSY	396	-
YSAELPKPS	2081	TIVTSAELPKPSISS	410	-
FTCEPEAQN	2082	AVAFTCCEPEAQNTTY	493	-
VTLDVLYGP	2083	SDPVTLDVLYGPDTTP	518	-
YGPDTPIIS	2084	DVLYGPDTPIISPD	582	-
		1937	588	0.0037

most common

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Table XXa CEA DR 3<sup>a</sup> Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
IQNDTGFYT	2067	QNIHQNDTGFYTLLHV	1920	0.3600	-0.0017	-0.0009		
IKSDLVNEE	2068	IHKVKSDLVNEEATG	1921					
LVNEEATGQ	2069	KSDLVNEEATGQFRV	1922					
VNEEATGQF	2070	SDLVNEEATGQFRVY	1923					
VYPELPKPS	2071	QFRVYPELPKPSISS	1924					
FTCEPETQD	2072	AVAFTEPETQDATY	1925					
YKCETQNPKV	2073	TASYKCETONPVSAR	1926					
YGPDAFTIS	2074	NVL YGPDAFTISPLN	1927					
VYAEPPKPF	2075	TITVVAEPPPKPITS	1928					
VEDEADAVAL	2076	SNPVEDEADAVALTCE	1929					
LTCPEPIQN	2077	AVALTCPEIQNNTY	1930					
IQNELSVDH	2078	ECGIONELSVDHSDP	1931					
LSVDHSDPV	2079	QNEL_SVDHSDPVILN	1932					
YGPDDPTIS	2080	NVL YGPDDPTISPY	1933					
VSAELPKPS	2081	TITVSAELPKPSISS	1934					
FTCEPEAQN	2082	AVAFTEPEAQNTY	1935					
VTLDVLYGP	2083	SDPVTLVDVLYGPDT	1936					
YGPDTPIIS	2084	DVL YGPDTPIISPD	1937					

CEA DR 3<sup>a</sup> Motif Peptides with Binding Data

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1934</p



Table XXb CEA DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Position	DRI	DR2w261	DR2w282	DR3	DR4w4	DR4w5	DR5w11	DR5w12
ATGQFRVYP	2085	NEEATGQFRVYPPELP	938	131						-0.0027	
LNTSYRSGE	2086	ISPLNTSYRSGENLN	1939	242						-0.0027	
YTCAQAHNSD	2087	SGSYTCQAHNSDTGL	1940	294						-0.0027	
LPVSPRLQL	2088	NQSLPVSPRLQLSND	1941	360						0.0071	
LSNDNRTLT	2089	RLOQNNDNRTLTLLS	1942	368	0.0001	-0.0006	-0.0007			0.3200	-0.0055
LSSCHAAS	2090	GVNLNSUCHSAAASNPP	1943	430						0.0075	
LNLSCHSAS	2091	GANLNLSUCHSASNPS	1944	608						-0.0027	
ASPETHLDM	2092	RLPASPETHLDMLRH	1945	34						-0.0027	
AHNQVROQP	2093	VLAHNQVROVPLQR	1946	84						0.0290	
LIDTNRSRA	2094	ALTLIDTNRSRACHP	1947	180						0.0350	
IHHNTHLCF	2095	LALIHNNTHLCFVHT	1948	465	0.0140	0.0590	0.0009			0.3100	-0.0055
LFRNPHQAL	2096	WDOLFRNPHQALLHT	1949	482	-0.0001	0.0015	-0.0007			0.9000	-0.0055
VDDDKCQP	2097	HSCVDLDDKGCPAEQ	1950	632						-0.0027	
YLEDYRLVH	2098	GMSYLEDVRLVHDL	1951	832						0.1800	
IDSECRPREF	2099	CWMIDSECRPREFREL	1952	958	0.0036	-0.0006	0.0150			0.4500	-0.0055
AAQPQHPPP	2100	QGGAAPQHPPPAFS	1953	1200						-0.0025	
AAISRKMVE	2101	EFQAAISRKMKMVELVH	1954	104						0.0039	
LHHTLKGIG	2102	VKVLHHTLKGIGEPH	1955	284						-0.0025	
IGGEPHISY	2103	TLKIGGEPHISYPL	1956	290						-0.0025	
AALSRKVAE	2104	EFQAAALSRKVAELVH	1957	104						0.0027	
ILGDPKILL	2105	EDSILGDPKILLTQH	1958	235	0.0003	-0.0006	-0.0010			0.6700	-0.0055
YKQSQHMTE	2106	MAIYKQSQHMTEVVR	1959	160						-0.0025	
VEGNLRYEVY	2107	LIRVEGNLRYEVYDD	1960	194						0.0930	
FTLQIRGRE	2108	GEYFTLQIRGREFE	1961	325						0.0290	

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Table XXb

CEA DR 3b Motif Peptides with Binding Data

Core Sequence	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9
ATGQFRVYP	2085	NEEATGQFRVYPPELP	1938			
LNTSYRSGE	2086	ISPLNTSYRSGENLN	1939			
YTCAHNSD	2087	SGSYTCQAHNSDTGL	1940			
LPVSPRLQL	2088	NOSLPVSPRLQLSDN	1941			
LSNDNRTLT	2089	RLQLSNDNRTLTLLS	1942			
LSSLCHAAS	2090	GVNLISLSCHAASNPP	1943			
LNLSCHSAS	2091	GANLNLSCHSASNPS	1944			
ASPETHLDM	2092	RLPASPETHLDMLRH	1945			
AHNQVROYP	2093	VLAHNQVROYPLQR	1946			
LIDTNRSA	2094	ALTLIDTNRSAACHP	1947			
IHHNTHLCF	2095	LALIHNNTHLCFVHT	1948			
LFRNPHQAL	2096	WDOLFRNPHQALLHT	1949			
VDLDDKGCP	2097	HSCVDLDDKGCPAEQ	1950			
YLEDVRLVH	2098	GMSYLEDVRLVHDL	1951			
IDSECRPRF	2099	CWMIDSECRPRFREL	1952			
AAPOPHPPP	2100	QGGAAPOPHPPPAFS	1953			
AAISRKMVE	2101	EFQAAISRKMVEVLVH	1954			
LHHTLKGIG	2102	VKVLHHTLKGIGEPH	1955			
IGGEPHISY	2103	TLKIGGEPHISYPL	1956			
AALSRKVAE	2104	EFQAAALSRKVAEVLVH	1957			
ILGDPKKLL	2105	EDSILGDPKKLLTQH	1958			
YKQSOHMTTE	2106	MAIYQSOHMTTEVVR	1959			
VEGNLRLVEYLD	2107	LIRVEGNLRLVEYLD	1960			
FTLQIRGRE	2108	GEYFTLQIRGRE	1961			

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Table XXII. Cross-reactive binding of CEA analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Bound
CEA.24	9	LLTFWNPPPT	2144	179	1720	67	755	-- <sup>2</sup>	2
CEA.24M2V9	9	LMTFWNPPV	2145	4.5	782	7.7	34	3333	3
CEA.24V9	9	LLTFWNPPV	2146	16	307	26	56	952	4
CEA.78	9	QIIGYVIGT	2147	313	148	106	100	150	5
CEA.78L2V9	9	QLIGYVIGV	2158	9.4	5.9	2.3	21	2.3	5
CEA.233	10	VLYGPDAPTI	2149	128	606	270	804	--	2
CEA.233V10	10	VLYGPDAPTV	2150	26	430	16	206	952	4
CEA.411	10	VLYGPDPTI	2151	294	358	476	7400	--	3
CEA.411V10	10	VLYGPDPTV	2152	161	105	91	2467	--	3
CEA.569	9	YVCGIQNSV	2153	98	358	159	80	181	5
CEA.569L2	9	YLCGIQNSV	2154	50	24	12	31	3478	4
CEA.589	9	VLYGPDPTI	2155	200	878	53	638	--	2
CEA.589V9	9	VLYGPDPTV	2156	20	165	91	154	9756	4
CEA.605	9	YLSGANLNL	2157	28	165	2.4	804	--	3
CEA.605V9	9	YLSGANLNV	2158	73	13	13	80	1600	4
CEA.687	9	ATVGIMIGV	2159	36	8.8	20	11	0.80	5
CEA.687L2	9	ALVGIMIGV	2160	10	63	31	100	102	5
CEA.691	9	IMIGVLVGV	2161	69	62	13	106	89	5
CEA.691L2	9	ILIGVLVGV	2162	22	8.0	3.2	16	160	5

1) Wild-type peptides presented for reference purposes.

2) -- indicates binding affinity = 10,000nM.

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TABLE XXII A A01 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	<u>A*0101 nM</u>
52.0105	11	RVDGNRQIIGY	2163	CEA.72	294.1
52.0109	11	RSDSVILNVLY	2164	CEA.225	47.2
52.0113	11	HSDPVILNVLY	2165	CEA.403	25.8
52.0116	11	RSDPVTLVDVLY	2166	CEA.581	7.8
57.0004	9	QQDTPGPAY	2167	CEA.87.D3	56.8
57.0007	9	AADNPPAQY	2168	CEA.261.D3	45.5
57.0008	9	ITDNNNSGSY	2169	CEA.289.D3	96.2
57.001	9	VTDNDVGPY	2170	CEA.383.D3	4.1
57.0011	9	PTDSPSYTY	2171	CEA.418.D3	37.9
57.0012	9	TIDPSYTYY	2172	CEA.419.D3	3.1
57.0013	9	AADNPPAQY	2173	CEA.439.D3	44.6
57.0014	9	ITDKNSGLY	2174	CEA.467.D3	11.9
57.0103	10	PTDSPLNTSY	2175	CEA.240.D3	266
57.0104	10	PTDSPSYTYY	2176	CEA.418.D3	1.1
57.0105	10	HTASNPSPQY	2177	CEA.616.T2	131.6
57.0106	10	HSDSNPSPQY	2178	CEA.616.D3	44.6

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Table XXII B A03 Analog Peptides

Peptide	AA	SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3_XRN
1371.01	10	TVSPLNNTSYR	2179	CEA.241.V2	458.3	54.5	187.5	557.7	8.7
1371.02	10	TVSPLNNTSYK	2180	CEA.241.V2K10	16.9	6.3	10588.2	-48333.3	7.3
1371.03	10	RVLTLLSVTR	2181	CEA.376.V2	343.8	222.2	11.3	6041.7	666.7
1371.04	10	RVLTLLSVTK	2182	CEA.376.V2K10	37.9	50	163.6	-72500	5714.3
1371.05	10	TVSPSYTYYR	2183	CEA.419.V2	2340.4	3000	29	263.6	8.6
1371.06	10	TVSPSYTYYK	2184	CEA.419.V2K10	68.8	42.9	3673.5	26363.6	6.7
1371.07	9	IVPSYTYYR	2185	CEA.420.V2	91.7	13.3	25.7	58	2.6
1371.08	9	IVPSYTYYK	2186	CEA.420.V2K9	17.2	54.5	720	4328.4	21.6
1371.09	10	RVLTLFNVTR	2187	CEA.554.V2	297.3	93.8	9	7631.6	42.1
1371.10	10	RVLTLFNVTK	2188	CEA.554.V42K10	20.8	31.6	233.8	41428.6	2352.9
1371.13	9	FVSNLATGK	2189	CEA.656.K9	1466.7	206.9	-36000	-72500	5.3

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aaQ



Table XXIIC A24 Analog Peptides

<u>Peptide</u>	<u>AA</u>	<u>Sequence</u>	<u>SEQ ID NO:</u>	<u>Source</u>	<u>A*2401 nM</u>
52.0033	8	IYPNASLL	2190	CEA.101	176.5
52.0038	8	SWFVNNGTF	2191	CEA.270	480
52.0137	11	RWCIPWQRLLL	2192	CEA.10	151.9
52.0138	11	PWQRLLLTAISL	2193	CEA.14	324.3
52.0141	11	FYTLHVIKSDL	2194	CEA.119	480
52.0142	11	TYLWWVNNQSQL	2195	CEA.175	85.7
52.0144	11	TYLWWVNNQSQL	2196	CEA.353	46.2
52.0145	11	SYTYYRPGVNL	2197	CEA.423	218.2
52.0146	11	TYYRPGVNLSL	2198	CEA.425	131.9
52.0147	11	TYLWWVNGQSL	2199	CEA.531	92.3
57.0036	9	RYCIPWQRF	2200	CEA.10.Y2F9	190.5
57.0037	9	IYPNASLLF	2201	CEA.101.F9	2.2
57.0038	9	LYWVNNQSF	2202	CEA.177.Y2F9	63.2
57.0039	9	LYGPDAPTF	2203	CEA.234.F9	63.2
57.0041	9	TYYRPGVNF	2204	CEA.425.F9	52.2
57.0042	9	LYWVNGQSF	2205	CEA.533.Y2F9	15.8
57.0044	9	QYSWRINGF	2206	CEA.624.F9	109.1
57.0045	9	TYACFVSNF	2207	CEA.652.F9	8.6
57.0072	10	RYCIPWQRLF	2208	CEA.10.Y2F10	26.1
57.0073	10	FYNPPPTTAKF	2209	CEA.27.Y2F10	181.8
57.0074	10	VYPELPKPSF	2210	CEA.140.F10	106.2
57.0075	10	TYQQSTQELF	2211	CEA.276.Y2	307.7
57.0076	10	VYAEPPKPFF	2212	CEA.318.F10	26.7
57.0077	10	YYRPGVNLSF	2213	CEA.426.F10	10
57.0078	10	QYSWLDGNF	2214	CEA.446.F10	60
57.0079	10	SYLGGANLNF	2215	CEA.604.F10	10

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Table XXIII. Immunogenicity of A2 supermotif-bearing peptides

Peptide	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*0802 nM	No. A2 Alleles Bound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
CEA.78	9	QILGYVIGT	2216	313	148	106	100	151	5	0/3		
CEA.354	10	YLWWVVNNQSL	2217	26	108	26	487	333	5	1/2	0/1	
CEA.569	9	YVCGIQNSV	2218	98	358	159	80	182	5	1/2	0/1	
CEA.605	9	YLSGANLNL	2219	28	165	2	804	.. <sup>2</sup>	3	2/2	1/2	
CEA.687	9	ATVGIMIGV	2220	36	9	20	11	1	5	1/1	1/1	
CEA.691	9	IMIGVLYGV	2221	69	62	13	106	89	5	8/8	4/7	
CEA.24	9	LLTFWNPP	2222	179	1720	67	755	.. <sup>2</sup>	2	0/1	0/1	
CEA.24V9	9	LLTFWNPPV	2223	16	307	26	56	952	4	1/1	1/1	
CEA.233	10	VLYGPDAPTI	2224	128	606	270	804	..	2	2/4	0/3	
CEA.233V10	10	VLYGPDAPTV	2225	26	430	16	206	952	4	3/4	2/2	1/4
CEA.589	9	VLYGPDTP1	2226	200	878	53	638	..	2	1/1	0/1	
CEA.589V9	9	VLYGPDTPV	2227	20	165	91	154	9756	4	2/2	2/2	0/2
CEA.605	9	YLSGANLNL	2228	28	165	24	804	..	3	2/2	1/2	
CEA.605V9	9	YLSGANLNV	2229	73	13	13	80	1600	4	4/4	3/4	1/4

1) Number of donors yielding a positive response/total tested.  
 2) .. indicates binding affinity = 10,000nM.

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Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

## A. Class I binding assays

Species	Antigen	Allele	Cell line	Source	Radio-labeled peptide	SEQ ID NO:
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	2230
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFFSV	2231
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFFSV	2232
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFFSV	2233
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFFSV	2234
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFFSV	2235
	A3	GM3107		KVFPYALINK	KVFPYALINK	2236
A11		BVR		KVFPYALINK	KVFPYALINK	2237
A24	A*2402	KAS116		AYIDNLYNKF	AYIDNLYNKF	2238
A31	A*3101	SPACH		KVFPYALINK	KVFPYALINK	2239
A33	A*3301	LWAGS		KVFPYALINK	KVFPYALINK	2240
A28/68	A*3801	CIR		STLPETVYVRR	STLPETVYVRR	2241
A28/68	A*3802	AMAI		FTQAGYPAL	FTQAGYPAL	2242
B7	B*0702	GM3107		APRTLVYLL	APRTLVYLL	2243
B8	B*0801	Steinlin		FLKDYQLL	FLKDYQLL	2244
B27	B*2705	LG2		FRYNGLHR	FRYNGLHR	2245
B35	B*3501	C1R, BVR		PPFKYAAAF	PPFKYAAAF	2246
B35	B*3502	TISI		PPFKYAAAF	PPFKYAAAF	2247
B35	B*3503	EHM		PPFKYAAAF	PPFKYAAAF	2248
B44	B*4403	PITOUT		AEMGKYSFY	AEMGKYSFY	2249
B51	B*5501	KAS116		PPFKYAAAF	PPFKYAAAF	2250
B53	B*5501	AMAI		PPFKYAAAF	PPFKYAAAF	2251
B54	B*5401	KT3		QYDDAVYKL	QYDDAVYKL	2252
Cw4	Cw*0401	C1R		YRHDDGGNVL	YRHDDGGNVL	2253
Cw6	Cw*0602	721.221 transfected		YRHDDGGNVL	YRHDDGGNVL	2254
Cw7	Cw*0702	721.221 transfected				2255
Mouse	D <sup>b</sup>	EL4		Adenovirus E1A P7->Y	SGPSNTYPEI	2256
	K <sup>b</sup>	EL4		VSV NP 52-59	RGYVFQGL	2257
	D <sup>d</sup>	P815		HIV-IIIB ENV G4->Y	RGPYRAFTI	2258
	K <sup>d</sup>	P815		non-natural (KdCON1)	KFNPMKTYI	2259
	L <sup>d</sup>	P815		HBV <sub>s</sub> 28-39	IPQSLDSYYWTL	2260



## B. Class II binding assays

Species	Antigen	Allele	Cell line	Radiolabeled peptide		
				Source	Sequence	SEQ ID NO:
Human	DR1	DRB1*0101	LG2	HA Y307-319	YPKYYVKQNTLKLAT	2261
	DR2	DRB1*1501	L466.1	MBP 88-102Y	VVFFFKNIVTPRTTPY	2262
	DR2	DRB1*1601	L242.5	non-natural (760.16)	YAFAAAAKTAAFAA	2263
	DR3	DRB1*0301	MAT	MT 65KD Y3-13	YKTIAFDEEAR	2264
	DR4w4	DRB1*0401	Preiss	non-natural (717.01)	YARFQSQTTLKQKT	2265
	DR4w10	DRB1*0402	YAR	non-natural (717.10)	YARFQRQTTLKAAA	2266
	DR4w14	DRB1*0404	BIN 40	non-natural (717.01)	YARFQSQTTLKQKT	2267
	DR4w15	DRB1*0405	KT3	non-natural (717.01)	YARFQSQTTLKQKT	2268
	DR7	DRB1*0701	Pitout	Tet. tox. 830-843	QYIKANSKFGFITE	2269
	DR8	DRB1*0802	OLL	Tet. tox. 830-843	QYIKANSKFGFITE	2270
	DR8	DRB1*0803	LUY	Tet. tox. 830-843	QYIKANSKFGFITE	2271
	DR9	DRB1*0901	HD	Tet. tox. 830-843	QYIKANSKFGFITE	2272
	DR11	DRB1*1101	Sweig	Tet. tox. 830-843	QYIKANSKFGFITE	2273
	DR12	DRB1*1201	Herluf	unknown eluted peptide	EAЛИHQQLKINPVVL	2274
	DR13	DRB1*1302	H0301	Tet. tox. 830-843 S->A	QYIKANAKFGFITE	2275
	DRS1	DRB5*0101	GM3107 or L416.3		QYIKANAKFGFITE	2276
	DRS1	DRB5*0201	L255.1	HA 307-319	PKYYVKQNTLKLAT	2277
	DRS2	DRB3*0101	MAT	Tet. tox. 830-843	NGQIGNDPNDL	2278
	DRS3	DRB4*0101	L257.6	non-natural (717.01)	YARFQSQTTLKQKT	2279
	DQ3.1	QAA1*0301/DQB1*0301	PF	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2280
Mouse	IA <sup>b</sup>		DB27.4	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2281
	IA <sup>a</sup>		A20	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2282
	IA <sup>a</sup>		CH-12	HEL 46-61	YNTDGSTDYGLQINSR	2283
	IA <sup>a</sup>		LS102.9	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2284
	IA <sup>a</sup>		91.7	non-natural (ROIV)	YAHAAHAAHAAHAAHAA	2285
	IE <sup>d</sup>		A20	Lambda repressor 12-26	YLEDARRKKKAIYEKKK	2286
	IE <sup>a</sup>		CH-12	Lambda repressor 12-26	YLEDARRKKKAIYEKKK	2287

add add



Table XXVI. Crossbinding data of A2 supermotif peptides.

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles	Crossbound
CEA.24	9	LLTFWNPP	2288	179	1720	67	755	--	2	
CEA.78	9	QIIGYVIGT	2289	313	148	106	100	150	5	
CEA.233	10	VLYGPDAPTI	2290	128	606	270	804	--	2	
CEA.354	10	YLWWVNNQSL	2291	26	108	26	487	67	5	
CEA.411	10	VLYGPDPTI	2292	294	358	476	7400	--	3	
CEA.432	9	NLSLSCHAA	2293	455	2867	1449	18500	--	1	
CEA.532	10	YLWWVNGQSL	2294	33	331	21	2056	286	4	
CEA.569	9	YVCGIQNSV	2295	98	358	159	80	181	5	
CEA.589	9	VLYGPDPTI	2296	200	878	53	638	--	2	
CEA.605	9	YLSGANLNL	2297	28	165	2.4	804	--	3	
CEA.687	9	ATVGIMIGV	2298	36	8.8	20	11	0.80	5	
CEA.690	10	GIMIGVLYGV	2299	64	205	31	142	500	5	
CEA.691	9	IMIGVLYGV	2300	69	62	13	106	89	5	
CEA.691	10	IMIGVLYGVA	2301	227	68	44	726	1509	3	

-- indicates binding affinity = 10,000nM.

*acted*



Table XXVII. Immunogenicity of A2 supermotif peptides

1) Number of donors yielding a positive response/total tested.

2) == indicates binding affinity = 10,000nM.



Table XXVIII. Immunogenicity A2 supermotif analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles	CTL Crossbound	CTL Peptide <sup>1</sup>	CTL Wild-type	CTL Tumor
CEA.24	9	LLTFWNPPPT	2308	179	1720	67	755	-- <sup>2</sup>	2		0/1	0/1	0/1
CEA.24V9	9	LLTFWNPPPV	2309	16	307	26	56	952	4	1/1			1/1
CEA.233	10	VLYGPDAPI	2310	128	606	270	804	--	2		2/4		0/3
CEA.233V10	10	VLYGPDAPTV	2311	26	430	16	206	952	4	3/4	2/2		1/4
CEA.589	9	VLYGPDTPI	2312	200	878	53	638	--	2		1/1		
CEA.589V9	9	VLYGPDTPV	2313	20	165	91	154	9756	4	2/2	2/2		0/2
CEA.605	9	YLSGANLNL	2314	28	165	2.4	804	--	3		2/2		1/2
CEA.605V9	9	YLSGANLNV	2315	73	13	13	80	1600	4	4/4	3/4		1/4

1) Number of donors yielding a positive response/total tested.  
 2) -- indicates binding affinity = 10,000nM.

*Added*



Table XXIX. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- reactivity
39.0217	2	RWCIPWQRLLLTLASL	2316	CEA.10	8.2	542	357	3
39.0218	3	QRLLLTAASLLTFWNP	2317	CEA.16	--	--	--	0
39.0219	2	EVLLLVHNLQPQHLFG	2318	CEA.50	2.0	52	53	3
39.0220	3	GREHYPNASLLIQN	2319	CEA.97	8.1	484	45	3
39.0221	2	EHYPNASLLIQNII	2320	CEA.99	14	1154	156	2
39.0222	2	NASLLIQNIIQNDTG	2321	CEA.104	4546	--	--	0
39.0223	3	DTGFYTLHVIKSDLV	2322	CEA.116	69	1731	227	2
39.0224	2	YPELPKPSISSNNSK	2323	CEA.141	5556	--	--	0
39.0225	2	KPSISSNNSKPVEDK	2324	CEA.146	2381	--	7576	0
39.0226	3	YLWWVNNQSLPVSPR	2325	CEA.176	0.59	8.0	42	3
39.0227	3	LWWVNNQSLPVSPRL	2326	CEA.177	217	1552	3049	1
39.0228	2	QYSWFVNQTFQQSTQ	2327	CEA.268	192	80	926	3
39.0229	2	DTGLNRTTVTTITVY	2328	CEA.305	--	--	2841	0
39.0230	2	KPFIITSNNNSNPVEDE	2329	CEA.324	--	--	--	0
39.0231	2	NRTLTLLSVTRNDVG	2330	CEA.375	238	--	--	1
39.0232	2	QELFISNITEKNSGL	2331	CEA.460	--	2500	--	0
39.0233	3	RTTVKTTIVSAELPK	2332	CEA.488	455	7031	317	2
39.0234	2	SAELPKPSISSNNSK	2333	CEA.497	--	--	--	0
39.0235	2	LDVLYGPDTPIISPP	2334	CEA.587	--	--	--	0
39.0236	2	TQVLFIAKITPNNNG	2335	CEA.637	61	--	6579	1
39.0237	2	QVLFIAKITPNNNGT	2336	CEA.638	42	1875	--	1
39.0238	3	YACFVSNLATGRNNS	2337	CEA.653	208	1667	3571	1
39.0239	2	NNSIVKSITVSASGT	2338	CEA.665	91	25	676	3
39.0240	3	NSIVKSITVSASGTS	2339	CEA.666	78	25	329	3

-- indicates binding affinity =10,000nM.

*add add*



Table XXX DR supertype crossbinding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2B1 nM	DR2w2B2 nM	DR6w19 nM	DR5w11 nM	DR8w2 nM	DR147 Degen	Broad Degen (5/8)
39.0217	RWCIPWQRULLTASL	2340	CEA.10	8.2	542	357	827	--	318	--	--	3	5
39.0219	EVLLLVHNLPQHLFG	2341	CEA.50	2.0	52	53	40	--	1.0	588	408	3	7
39.0220	GREIYPNASSLIQN	2342	CEA.97	8.1	484	45	24	8333	2.9	6897	5904	3	5
39.0221	EIYPNASSLIQNI	2343	CEA.99	14	1154	156	57	--	11	--	--	2	4
39.0223	DTGFTYTLHVIKSDLV	2344	CEA.116	69	1731	227	506	800	3889	2500	790	2	5
39.0226	YLWWVNNQSLPVSPR	2345	CEA.176	0.60	8.0	42	110	2105	2.3	29	1065	3	6
39.0228	QYSWFVNQGTQQSTQ	2346	CEA.268	192	80	926	--	6061	5833	370	--	3	4
39.0233	RTTVKTITVSAELPK	2347	CEA.488	455	7031	317	364	--	700	--	--	2	4
39.0239	NNSIVKSITVSASGT	2348	CEA.665	91	25	676	3138	--	51	--	4083	3	4
39.0240	NSIVKSITVSASGTS	2349	CEA.666	78	25	329	3957	--	76	--	2882	3	4

-- indicates binding affinity = 10,000nM.



Table XXXI. DR3 binding

Peptide	Sequence	SEQ ID NO:	Source	DR3 nM
39.0313	QNIIQNDTGFYTLHV	2350	CEA.110	938
39.0314	LHVIKSDLVNEEATG	2351	CEA.122	2308
39.0315	KSDLVNEEATGQFRV	2352	CEA.126	--
39.0316	SDLVNEEATGQFRVY	2353	CEA.127	--
39.0317	NEEATGQFRVYPELP	2354	CEA.131	--
39.0318	QFRVYPELPKPSISS	2355	CEA.137	--
39.0319	AVAFTCPEPETQDATY	2356	CEA.162	--
39.0320	TASYKCETQNPVSAR	2357	CEA.210	--
39.0321	NVLYGPDAPTISPLN	2358	CEA.232	--
39.0322	ISPLNTSYRSGENLN	2359	CEA.242	--
39.0323	SGSYTCQAHNSDTGL	2360	CEA.294	--
39.0324	TITVYAEPPKPFITS	2361	CEA.315	--
39.0325	SNPVEDEDAVALTCE	2362	CEA.332	--
39.0326	AVALTCEPEIQNTTY	2363	CEA.340	--
39.0327	NQSLPVSPRLQLSND	2364	CEA.360	--
39.0328	RLQLSNDNRTLTLLS	2365	CEA.368	938
39.0329	ECGIQNELSVDHSDP	2366	CEA.392	--
39.0330	QNELSVDHSDPVILN	2367	CEA.396	3659
39.0331	NVLYGPDDPTISPY	2368	CEA.410	--
39.0332	GVNLSSLSCHAASNPP	2369	CEA.430	--
39.0333	TITVSAELPKPSISS	2370	CEA.493	--
39.0334	AVAFTCPEAQNTTY	2371	CEA.518	--
39.0335	SDPVTLVDVLYGPDT	2372	CEA.582	--
39.0336	DVLYGPDTPIISPPD	2373	CEA.588	--
39.0337	GANLNLSCHSASNPS	2374	CEA.608	--

-- indicates binding affinity = 10,000nM.



Table XXXII. HTLCandidate Epitopes

Peptide	Sequence	SEQ ID NO:	Motif	Source	DR1 nM	DR4w4 nM	DR7 nM	DR3 nM	DR2w2 $\beta$ 1 nM	DR2w2 $\beta$ 2 nM	DR5w1 1 nM	DR8w2 nM	DR147 Cross-reactivity	Broad Cross-reactivity (5/8)	DR3 Binder
39.0217	RWCIFPWQRULLTASL	2375	DR sup	CEA.10	8.2	542	357	--	827	--	318	--	--	3	5
39.0219	EVLLLVHNLPQHLLFG	2376	DR sup	CEA.50	2.0	52	53	336	40	--	1.0	588	408	3	7
39.0220	GREIIYPNANSLLIQN	2377	DR sup	CEA.97	8.1	484	45	1123	24	8333	2.9	6897	5904	3	5
39.0313	QNIIQQQNDTGFYTLHV	2378	DR3	CEA.110	1136	>8182	--	938	867	--	9.7	--	--	0	2
39.0223	DTGFTYTLHVIKSDLV	2379	DR sup	CEA.116	69	1731	227	--	506	800	3889	2500	790	2	5
39.0226	YLWWVNNQSLPVSPR	2380	DR sup	CEA.176	0.60	8.0	42	2310	110	2105	2.3	29	1065	3	6
39.0328	RLQLSNDNRRTLTLSS	2381	DR3	CEA.368	--	>8182	--	938	--	--	729	--	--	0	1

-- indicates binding affinity = 10,000nM

90000